

SEQUENCE LISTING

<110> INCYTE PHARMACEUTICALS, INC.

BANDMAN, Olga

TANG, Y. Tom

CORLEY, Neil C.

AZIMZAI, Yalda

BAUGHN, Mariah R.

<120> HUMAN SCAD-RELATED MOLECULES, SCRM-1 AND SCRM-2

<130> PF-0559 USN

<140> 09/743,752

<141> Herewith

<150> PCT/US9916164

<151> 1999-07-16

<150> US 09/116,750

<151> 1998-07-16

<150> US 60/160,074

<151> 1998-07-16

<160> 6

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 278

<212> PRT

<213> HOMO SAPIENS

<220>

<221> misc_feature

<223> Incyte Clone No: 1240869

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Val	Arg	Met	Ala	Ser	Ser	Arg	Met	Thr	Arg	Arg	Asp	Pro	Leu	Thr	Asn
			20					25					30		
Lys	Val	Ala	Leu	Val	Thr	Ala	Ser	Thr	Asp	Gly	Ile	Gly	Phe	Ala	Ile
		35					40					45			
Ala	Arg	Arg	Leu	Ala	Gln	Asp	Arg	Ala	His	Val	Val	Val	Ser	Ser	Arg
		50				55					60				
Lys	Gln	Gln	Asn	Val	Asp	Gln	Ala	Val	Ala	Thr	Leu	Gln	Gly	Glu	Gly
65					70					75				80	
Leu	Ser	Val	Thr	Gly	Thr	Val	Cys	His	Val	Gly	Lys	Ala	Glu	Asp	Arg
			85						90					95	
Glu	Arg	Leu	Val	Ala	Thr	Ala	Val	Lys	Leu	His	Gly	Gly	Ile	Asp	Ile
			100					105					110		
Leu	Val	Ser	Asn	Ala	Ala	Val	Asn	Pro	Phe	Phe	Gly	Ser	Ile	Met	Asp
			115				120						125		

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Val Thr Glu Glu Val Trp Asp Lys Thr Leu Asp Ile Asn Val Lys Ala
 130                      135                      140
Pro Ala Leu Met Thr Lys Ala Val Val Pro Glu Met Glu Lys Arg Gly
145                      150                      155                      160
Gly Gly Ser Val Val Ile Val Ser Ser Ile Ala Ala Phe Ser Pro Ser
                      165                      170                      175
Pro Gly Phe Ser Pro Tyr Asn Val Ser Lys Thr Ala Leu Leu Gly Leu
                      180                      185                      190
Asn Asn Thr Leu Ala Ile Glu Leu Ala Pro Arg Asn Ile Arg Val Asn
                      195                      200                      205
Cys Leu Ala Pro Gly Leu Ile Lys Thr Ser Phe Ser Arg Met Leu Trp
210                      215                      220
Met Asp Lys Glu Lys Glu Glu Ser Met Lys Glu Thr Leu Arg Ile Arg
225                      230                      235                      240
Arg Leu Gly Glu Pro Glu Asp Cys Ala Gly Ile Val Ser Phe Leu Cys
                      245                      250                      255
Ser Glu Asp Ala Ser Tyr Ile Thr Gly Glu Thr Val Val Val Gly Gly
260                      265                      270
Gly Thr Pro Ser Arg Leu
275

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<210> 2

<211> 564

<212> PRT

<213> HOMO SAPIENS

<220>

<221> misc_feature

<223> Incyte Clone No: 2060002

<400> 2

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Tyr Ala Tyr Pro Ser Asp Tyr Asp Met His Thr Gly Asp Pro Lys Gln
20                      25                      30
Asp Leu Ala Tyr Glu Arg Gln Tyr Glu Gln Gln Thr Tyr Gln Val Ile
35                      40                      45
Pro Glu Val Ile Lys Asn Phe Ile Gln Tyr Phe His Lys Thr Val Ser
50                      55                      60
Asp Leu Ile Asp Gln Lys Val Tyr Glu Leu Gln Ala Ser Arg Val Ser
65                      70                      75                      80
Ser Asp Val Ile Asp Gln Lys Val Tyr Glu Ile Gln Asp Ile Tyr Glu
85                      90                      95
Asn Ser Trp Thr Lys Leu Thr Glu Arg Phe Phe Lys Asn Thr Pro Trp
100                      105                      110
Pro Glu Ala Glu Ala Ile Ala Pro Gln Val Gly Asn Asp Ala Val Phe
115                      120                      125
Leu Ile Leu Tyr Lys Glu Leu Tyr Tyr Arg His Ile Tyr Ala Lys Val
130                      135                      140
Ser Gly Gly Pro Ser Leu Glu Gln Arg Phe Glu Ser Tyr Tyr Asn Tyr
145                      150                      155                      160
Cys Asn Leu Phe Asn Tyr Ile Leu Asn Ala Asp Gly Pro Ala Pro Leu
165                      170                      175
Glu Leu Pro Asn Gln Trp Leu Trp Asp Ile Ile Asp Glu Phe Ile Tyr
180                      185                      190
Gln Phe Gln Ser Phe Ser Gln Tyr Arg Cys Lys Thr Ala Lys Lys Ser
195                      200                      205

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Glu	Glu	Glu	Ile	Asp	Phe	Leu	Arg	Ser	Asn	Pro	Lys	Ile	Trp	Asn	Val	210	215	220
His	Ser	Val	Leu	Asn	Val	Leu	His	Ser	Leu	Val	Asp	Lys	Ser	Asn	Ile	225	230	235
Asn	Arg	Gln	Leu	Glu	Val	Tyr	Thr	Ser	Gly	Gly	Asp	Pro	Glu	Ser	Val	245	250	255
Ala	Gly	Glu	Tyr	Gly	Arg	His	Ser	Leu	Tyr	Lys	Met	Leu	Gly	Tyr	Phe	260	265	270
Ser	Leu	Val	Gly	Leu	Leu	Arg	Leu	His	Ser	Leu	Leu	Gly	Asp	Tyr	Tyr	275	280	285
Gln	Ala	Ile	Lys	Val	Leu	Glu	Asn	Ile	Glu	Leu	Asn	Lys	Lys	Ser	Met	290	295	300
Tyr	Ser	Arg	Val	Pro	Glu	Cys	Gln	Val	Thr	Thr	Tyr	Tyr	Tyr	Val	Gly	305	310	315
Phe	Ala	Tyr	Leu	Met	Met	Arg	Arg	Tyr	Gln	Asp	Ala	Ile	Arg	Val	Phe	325	330	335
Ala	Asn	Ile	Leu	Leu	Tyr	Ile	Gln	Arg	Thr	Lys	Ser	Met	Phe	Gln	Arg	340	345	350
Thr	Thr	Tyr	Lys	Tyr	Glu	Met	Ile	Asn	Lys	Gln	Asn	Glu	Gln	Met	His	355	360	365
Ala	Leu	Leu	Ala	Ile	Ala	Leu	Thr	Met	Tyr	Pro	Met	Arg	Ile	Asp	Glu	370	375	380
Ser	Ile	His	Leu	Gln	Leu	Arg	Glu	Lys	Tyr	Gly	Asp	Lys	Met	Leu	Arg	385	390	395
Met	Gln	Lys	Gly	Asp	Pro	Gln	Val	Tyr	Glu	Glu	Leu	Phe	Ser	Tyr	Ser	405	410	415
Cys	Pro	Lys	Phe	Leu	Ser	Pro	Val	Val	Pro	Asn	Tyr	Asp	Asn	Val	His	420	425	430
Pro	Asn	Tyr	His	Lys	Glu	Pro	Phe	Leu	Gln	Gln	Leu	Lys	Val	Phe	Ser	435	440	445
Asp	Glu	Val	Gln	Gln	Gln	Ala	Gln	Leu	Ser	Thr	Ile	Arg	Ser	Phe	Leu	450	455	460
Lys	Leu	Tyr	Thr	Thr	Met	Pro	Val	Ala	Lys	Leu	Ala	Gly	Phe	Leu	Asp	465	470	475
Leu	Thr	Glu	Gln	Glu	Phe	Arg	Ile	Gln	Leu	Leu	Val	Phe	Lys	His	Lys	485	490	495
Met	Lys	Asn	Leu	Val	Trp	Thr	Ser	Gly	Ile	Ser	Ala	Leu	Asp	Gly	Glu	500	505	510
Phe	Gln	Ser	Ala	Ser	Glu	Val	Asp	Phe	Tyr	Ile	Asp	Lys	Asp	Met	Ile	515	520	525
His	Ile	Ala	Asp	Thr	Lys	Val	Ala	Arg	Arg	Tyr	Gly	Asp	Phe	Phe	Ile	530	535	540
Arg	Gln	Ile	His	Lys	Phe	Glu	Glu	Leu	Asn	Arg	Thr	Leu	Lys	Lys	Met	545	550	555
Gly	Gln	Arg	Pro															

<210> 3

<211> 1280

<212> DNA

<213> HOMO SAPIENS

<220>

<221> misc_feature

<223> Incyte Clone No: 1240869

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acaaataagg	tggccctggt	aacggcctcc	accgacggga	tcggcttcgc	catcgcccg	180
cgtttgccc	aggacagggc	ccacgtggtc	gtcagcagcc	ggaagcagca	gaatgtggac	240
caggcgggtg	ccacgctgca	gggggagggg	ctgagcgtga	cgggcaccgt	gtgccatgtg	300
gggaaggcgg	aggaccggga	gcggctggtg	gccacggctg	tgaagcttca	tggaggtatc	360
gatatcctag	tctccaatgc	tgctgtcaac	cctttctttg	gaagcataat	ggatgtcact	420
gaggaggtgt	gggacaagac	tctggacatt	aatgtgaagg	cccagccct	gatgacaaag	480
gcagtgggtg	cagaaatgga	gaaacgagga	ggcggctcag	tggtgatcgt	gtcttccata	540
gcagccttca	gtccatctcc	tggttccagt	ccttacaatg	tcagtaaaac	agccttgctg	600
ggcctcaaca	ataccctggc	catagagctg	gccccaaagga	acattagggg	gaactgccta	660
gcacctggac	ttatcaagac	tagcttcagc	aggatgctct	ggatggacaa	ggaaaaagag	720
gaaagcatga	aagaaaccct	gcggataaga	aggttaggcg	agccagagga	ttgtgctggc	780
atcgtgtctt	tcctgtgctc	tgaagatgcc	agctacatca	ctggggaaac	agtgggtggg	840
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ctctagctcc	tgggtgctgt	cctgcattca	cccactggcc	tttcccacct	ctgctcacct	960
tactgttcac	ctcatcaaat	cagttctgcc	ctgtgaaaag	atccagcctt	ccctgccgtc	1020
aaggtggcgt	cttactcggg	attcctgctg	ttgttggtgg	cctgggtaaa	ggcctcccct	1080
gagaacacag	gacaggcctg	ctgacaaggc	tgagtctacc	ttggcaaaga	ccaagatatt	1140
tttctctggg	ccactgggga	atctgagggg	tgatgggaga	gaaggaaact	ggagtgggaag	1200
gagcagagtt	gcaaattaac	aacttgcaaa	tgaggtgcaa	ataaaatgca	gatgattgcg	1260
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<210> 4

<211> 1894

<212> DNA

<213> HOMO SAPIENS

<220>

<221> misc_feature

<223> Incyte Clone No: 2060002

<400> 4

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gcttatgaac	gtcagtatga	acagcaaacc	tatcagggtga	tccctgaggt	gatcaaaaac	180
ttcatccagt	atttccacaa	aactgtctca	gatttgattg	accagaaagt	gtatgagcta	240
caggccagtc	gtgtctccag	tgatgtcatt	gaccagaagg	tgtatgagat	ccaggacatc	300
tatgagaaca	gctggaccaa	gctgactgaa	agattcttca	agaatacacc	ttggcccag	360
gctgaagcca	ttgctccaca	ggttggcaat	gatgctgtct	tcctgatttt	atacaaagaa	420
ttatactaca	ggcacatata	tgccaaagtc	agtgggggac	cttcccttga	gcagagggtt	480
gaatcctatt	acaactactg	caatctcttc	aactacattc	ttaatgccga	tggtcctgct	540
ccccttgaac	tacccaacca	gtggctctgg	gatattatcg	atgagttcat	ctaccagttt	600
cagtcattca	gtcagtagcg	ctgtaagact	gccaagaagt	cagaggagga	gattgacttt	660
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gtagacaaat	ccaacatcaa	ccgacagttg	gaggtataca	caagcggagg	tgaccctgag	780
agtgtggctg	gggagtatgg	gcggcactcc	ctctacaaaa	tgcttggtta	cttcagcctg	840
gtcgggcttc	tccgcctgca	ctccctgtta	ggagattact	accaggccat	caagggtgctg	900
gagaacatcg	aactgaacaa	gaagagtatg	tattcccgtg	tgccagagtg	ccaggtcacc	960
acatactatt	atgttgggtt	tgcatatttg	atgatgcgtc	gttaccagga	tgccatccgg	1020
gtcttcgcca	acatcctcct	ctacatccag	aggaccaaga	gcatgttcca	gaggaccacg	1080
tacaagtatg	agatgattaa	caagcagaat	gagcagatgc	atgcgctgct	ggccattgcc	1140
ctcacgatgt	accccatgcg	tatcgatgag	agcattcacc	tccagctgcg	ggagaaatat	1200
ggggacaaga	tggtgcgcat	gcagaaagg	gaccacaag	tctatgaaga	acttttcagt	1260
tactcctgcc	ccaagttcct	gtcgcctgta	gtgcccact	atgataatgt	gcaccccaac	1320
taccacaaag	agcccttcct	gcagcagctg	aagggtgttt	ctgatgaagt	acagcagcag	1380

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gccagcttt caaccatccg cagcttcctg aagctctaca ccaccatgcc tgtggccaag 1440
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cacaagatga agaacctcgt gtggaccagc ggtatctcag ccctggatgg tgaatttcag 1560
tcagcctcag aggttgactt ctacattgat aaggacatga tccacatcgc ggacaccaag 1620
gtcgccaggc gttatgggga tttcttcac cgtcagatcc acaaatttga ggagcttaat 1680
cgaacctga agaagatggg acagagacct tgatgatatt cacacacatt caggaacctg 1740
ttttgatgta ttataggcag gaagtgtttt tgcctaccgtg aaacctttac ctagatcagc 1800
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<210> 5

<211> 280

<212> PRT

<213> HOMO SAPIENS

<220>

<221> misc_feature

<223> GENBANK ID: g1079566

<400> 5

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      20           25           30
Val Leu Ala Asn Arg Val Ala Val Val Thr Gly Ser Thr Ser Gly Ile
      35           40           45
Gly Phe Ala Ile Ala Arg Arg Leu Ala Arg Asp Gly Ala His Val Val
      50           55           60
Ile Ser Ser Arg Lys Gln Gln Asn Val Asp Arg Ala Met Ala Lys Leu
      65           70           75           80
Gln Gly Glu Gly Leu Ser Val Ala Gly Ile Val Cys His Val Gly Lys
      85           90           95
Ala Glu Asp Arg Glu Gln Leu Val Ala Lys Ala Leu Glu His Cys Gly
      100          105          110
Gly Val Asp Phe Leu Val Cys Ser Ala Gly Val Asn Pro Leu Val Gly
      115          120          125
Ser Thr Leu Gly Thr Ser Glu Gln Ile Trp Asp Lys Ile Leu Ser Val
      130          135          140
Asn Val Lys Ser Pro Ala Leu Leu Leu Ser Gln Leu Leu Pro Tyr Met
      145          150          155          160
Glu Asn Arg Arg Gly Ala Val Ile Leu Val Ser Ser Ile Ala Ala Tyr
      165          170          175
Asn Pro Val Val Ala Leu Gly Val Tyr Asn Val Ser Lys Thr Ala Leu
      180          185          190
Leu Gly Leu Thr Arg Thr Leu Ala Leu Glu Leu Ala Pro Lys Asp Ile
      195          200          205
Arg Val Asn Cys Val Val Pro Gly Ile Ile Lys Thr Asp Phe Ser Lys
      210          215          220
Val Phe His Gly Asn Glu Ser Leu Trp Lys Asn Phe Lys Glu His His
      225          230          235          240
Gln Leu Gln Arg Ile Gly Glu Ser Glu Asp Cys Ala Gly Ile Val Ser
      245          250          255
Phe Leu Cys Ser Pro Asp Ala Ser Tyr Val Asn Gly Glu Asn Ile Ala
      260          265          270
Val Ala Gly Tyr Ser Thr Arg Leu
      275          280

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<210> 6
 <211> 938
 <212> PRT
 <213> CAENORHABDITIS ELEGANS

<220>
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 <223> GENBANK ID: g2731377

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 20 25 30
 Glu Val Ala Asp Tyr Leu Val Tyr Phe Ser Arg Met Val Asp Glu Gln
 35 40 45
 Asn Val Pro Glu Ile Leu Thr Leu Tyr Asp Gln Ala Phe Pro Asp Leu
 50 55 60
 Thr Glu Arg Phe Phe Arg Asp Arg Met Trp Pro Asp Glu Asn Val Val
 65 70 75 80
 Glu Arg Ile Ile Gly Pro Gly Asn Lys Leu Phe Ile Ile Leu Tyr Lys
 85 90 95
 Glu Leu Tyr Tyr Arg Gln Leu Tyr Ala Arg Asn Thr Arg Gly Pro Leu
 100 105 110
 Leu Val His Arg Tyr Glu Ser Phe Met Asn Tyr Gln Glu Leu Phe Ser
 115 120 125
 Glu Leu Leu Ser Ser Lys Asp Pro Ile Pro Leu Ser Leu Pro Asn Val
 130 135 140
 Trp Leu Trp Asp Ile Ile Asp Glu Phe Val Tyr Gln Phe Gln Ala Phe
 145 150 155 160
 Cys Leu Tyr Lys Ala Asn Pro Gly Lys Arg Asn Ala Asp Glu Val Glu
 165 170 175
 Asp Leu Ile Asn Ile Glu Glu Asn Gln Asn Ala Trp Asn Ile Tyr Pro
 180 185 190
 Val Leu Asn Ile Leu Tyr Ser Leu Leu Ser Lys Ser Gln Ile Val Glu
 195 200 205
 Gln Leu Lys Ala Leu Lys Glu Lys Arg Asn Pro Asp Ser Val Ala Asp
 210 215 220
 Glu Phe Gly Gln Ser Asp Leu Tyr Phe Lys Leu Gly Tyr Phe Ala Leu
 225 230 235 240
 Ile Gly Leu Leu Arg Thr His Val Leu Leu Gly Asp Tyr His Gln Ala
 245 250 255
 Leu Lys Thr Val Gln Tyr Val Asp Ile Asp Pro Lys Gly Ile Tyr Asn
 260 265 270
 Thr Val Pro Thr Cys Leu Val Thr Leu His Tyr Phe Val Gly Phe Ser
 275 280 285
 His Leu Met Met Arg Asn Tyr Gly Glu Ala Thr Lys Met Phe Val Asn
 290 295 300
 Cys Leu Leu Tyr Ile Gln Arg Thr Lys Ser Val Gln Asn Gln Gln Pro
 305 310 315 320
 Ser Lys Lys Asn Phe Gln Tyr Asp Val Ile Gly Lys Thr Trp Asp Gln
 325 330 335
 Leu Phe His Leu Leu Ala Ile Cys Leu Ala Ile Gln Pro Gln Arg Ile
 340 345 350
 Asp Glu Ser Ile Ala Ser Gln Leu Ser Glu Arg Cys Gly Glu Arg Met
 355 360 365
 Met His Met Ala Asn Gly Asn Ile Asp Glu Phe Arg Asn Ala Phe Ala

370	375	380
Thr Gly Cys Pro Lys Phe Leu Ser Pro Thr Thr Val Val Tyr Glu Gly		
385	390	395
Val Asn Gln Ser Lys Glu Pro Leu Leu Arg Gln Thr Gln Ser Phe Leu		400
	405	410
Glu Gly Ile Glu Ser Gln Met Ala Leu Pro Val Leu Arg Gly Tyr Leu		415
	420	425
Lys Leu Tyr Thr Thr Leu Pro Thr Lys Lys Leu Ala Ser Phe Met Asp		430
	435	440
Val Asp Asp Glu His Tyr Asp Ser Phe Ile Gly Lys Leu Leu Thr Tyr		445
	450	455
Lys Met Ile Val Asn Glu Leu Gly Lys Glu Ala Gly Pro Ser Ser Ala		460
465	470	475
Asp Asp Asp Glu Pro Gln Thr Asp Ile Asp Phe Tyr Val Asp Arg Asp		480
	485	490
Met Ile Asn Ile Ala Asp Thr Lys Val Ala Arg His Val Gly Cys Ala		495
	500	505
Gln Thr Thr Arg Tyr Pro Glu Thr Met Ile Leu Lys Lys Phe Val		510
	515	520
Gly Arg Thr Val Leu Ile Thr Gly Ala Ser Arg Gly Ile Gly Lys Glu		525
	530	535
Ile Ala Leu Lys Leu Ala Lys Asp Gly Ala Asn Ile Val Val Ala Ala		540
545	550	555
Lys Thr Ala Thr Ala His Pro Lys Leu Pro Gly Thr Ile Tyr Ser Ala		560
	565	570
Ala Glu Glu Ile Glu Lys Ala Gly Gly Lys Ala Leu Pro Cys Ile Val		575
	580	585
Asp Val Arg Asp Glu Ala Ser Val Lys Ala Ser Val Glu Glu Ala Val		590
	595	600
Lys Lys Phe Gly Gly Ile Asp Ile Leu Ile Asn Asn Ala Ser Ala Ile		605
	610	615
Ser Leu Thr Asp Thr Glu Asn Thr Glu Met Lys Arg Tyr Asp Leu Met		620
625	630	635
His Ser Ile Asn Thr Arg Gly Thr Phe Leu Met Thr Lys Thr Cys Leu		640
	645	650
Pro Tyr Leu Lys Ser Gly Lys Asn Pro His Val Leu Asn Ile Ser Pro		655
	660	665
Pro Leu Leu Met Glu Thr Arg Trp Phe Ala Asn His Val Ala Tyr Thr		670
	675	680
Met Ala Lys Tyr Gly Met Ser Met Cys Val Leu Gly Gln His Glu Glu		685
	690	695
Phe Arg Pro His Gly Ile Ala Val Asn Ala Leu Trp Pro Leu Thr Ala		700
705	710	715
Ile Trp Thr Ala Ala Met Glu Met Leu Ser Asp Lys Gly Gly Glu Ala		720
	725	730
Gly Ser Arg Lys Pro Ser Ile Met Ala Asp Ala Ala Tyr Ala Val Leu		735
	740	745
Ser Lys Asn Ser Lys Asp Phe Thr Gly Asn Phe Cys Ile Asp Glu Asp		750
	755	760
Ile Leu Lys Ala Glu Gly Val Thr Asp Phe Asp Arg Tyr Ala Cys Val		765
	770	775
Pro Asp Ala Pro Leu Met Pro Asp Phe Phe Ile Pro Ala Gly Thr Tyr		780
785	790	795
Asp His Lys Phe Ser Ser Gly Ala Gln Ile Gly Lys Lys Asn Lys Thr		800
	805	810
His Glu Ala Gly Val Val Glu Glu Glu Ile Lys Gln Ile Phe Thr Ser		815
	820	825
		830

Ala	Lys	Arg	Leu	Leu	Asn	Ala	Asp	Ile	Val	Lys	Lys	Thr	Gly	Phe	Val
	835						840						845		
Tyr	Glu	Phe	Leu	Leu	Lys	Asp	Pro	Thr	Thr	Lys	Ser	Glu	Arg	Ile	Ile
	850					855					860				
Thr	Leu	Asp	Leu	Lys	Asn	Gly	Glu	Gly	Ala	Leu	Thr	Asp	Lys	Lys	Ala
865					870					875					880
Ser	Gly	Lys	Ala	Asp	Val	Lys	Phe	Thr	Leu	Ala	Pro	Glu	His	Phe	Ala
				885					890					895	
Pro	Leu	Phe	Thr	Gly	Lys	Leu	Arg	Pro	Thr	Thr	Ala	Leu	Met	Thr	Lys
			900					905					910		
Lys	Leu	Gln	Ile	Ser	Gly	Asp	Met	Pro	Gly	Ala	Met	Lys	Leu	Glu	Ser
		915				920						925			
Leu	Leu	Arg	Lys	Phe	Thr	Glu	Gly	Lys	Leu						
	930					935									